

**AMENDMENT TO THE SPECIFICATION**

Please amend the specification as described below.

Please replace paragraphs [0209]-[0214] with the following paragraph.

--[0209] The nucleotide sequence of each of a plurality of GAM oligonucleotides that are described by Fig. 1 and their respective genomic sequences and genomic locations are set forth in Tables 1-3, hereby incorporated herein. Specifically, in Table 1, line 241237, GAM RNA (miRNA) as set forth in SEQ ID NO: 117937 is shown as predicted from human herpesvirus 5.

GAM	GAM NAME	GAM RNA SEQUENCE	GAM ORGANISM	GAM
SEQ-ID				POS
=====	=====	=====	=====	=====
117937	GAM501831	AGTGACGGTGAGATCCAGGCTG	Human herpesvirus 5	A

In Table 2, lines 4474648-4474741, describes GAM PRECURSOR RNA (hairpin) as set forth in SEQ ID NO: 4204050 and as it relates to Figures 1-8.

GAM NAME	GAM	PRECUR	PRECURSOR	GAM DESCRIPTION
	ORGANISM	SEQ-ID	SEQUENCE	
=====	=====	=====	=====	=====
GAM501831	Human herp	420405	GACAGCCTCC	Fig. 1 further provides a conceptual description of another novel,
	esvirus 5	0	GGATCACATG	bioinformatically-detected viral oligonucleotide of the present invention,
			GTTACTCAGC	encoded by the Human herpesvirus 5 genome, referred to here as the Genomic
			GTCTGCCAGC	Address Messenger 501831 (GAM501831) oligonucleotide, which modulates
			CTAAGTGACG	expression of respective target genes whose function and utility are known
			GTGAGATCCA	in the art.
			GGCTGTC	GAM501831 is a novel, bioinformatically detectable, regulatory,
				non-protein-coding, miRNA-like oligonucleotide. The method by which
				GAM501831 is detected is described with additional reference to Figs. 1-8.
				The GAM501831 precursor, herein designated GAM PRECURSOR, is encoded by the
				Human herpesvirus 5 genome, which is a DNA virus. GAM501831 target gene,
				herein designated GAM TARGET GENE, is a target gene encoded by a target
				organism specified in Tables 6-7.

The GAM501831 precursor, herein designated GAM PRECURSOR, encodes a GAM501831 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA oligonucleotides, the GAM501831 precursor RNA does not encode a protein.

GAM501831 precursor RNA folds onto itself, forming GAM501831 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional "hairpin" structure. As is well-known in the art, this "hairpin structure" is typical of RNA encoded by known miRNA precursor oligonucleotides and is due to the full or partial complementarity of the nucleotide sequence of the first half of an miRNA precursor to the nucleotide sequence of the second half thereof.

A nucleotide sequence that is identical or highly similar to the nucleotide sequence of the GAM501831 precursor RNA is designated SEQ ID NO:4204050, and is provided hereinbelow with reference to the sequence listing section.

The nucleotide sequence designated SEQ ID NO:4204050 is located from position 164118 to position 164184 relative to the source sequence NC\_001347 (GenBank, NCBI), on the "+" strand on the genome of Human herpesvirus 5... A schematic representation of a predicted secondary folding of GAM501831 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA is set forth in Table 4 incorporated herein.

An enzyme complex composed of Dicer RNaseIII together with other necessary proteins, designated DICER COMPLEX, cuts the GAM501831 folded precursor RNA yielding a single-stranded, ~22 nt-long RNA segment designated GAM501831 RNA, herein designated GAM RNA. Table 5 provides two possible nucleotide sequences of GAM501831 RNA: a nucleotide sequence that is highly likely to be identical or extremely similar to the nucleotide sequence of GAM501831 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM501831 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, designated GAM501831 target RNA, herein designated GAM TARGET RNA. As is typical of mRNA of a protein-coding gene, GAM501831 target RNA comprises three regions: a 5' untranslated region, a protein-coding region and a 3' untranslated region, designated 5'UTR, PROTEIN-CODING and 3'UTR, respectively.

GAM501831 RNA, herein designated GAM RNA binds complementarily to one or more target binding sites located in the untranslated regions of GAM501831 target RNA. This complementary binding is due to the partial or full complementarity between the nucleotide sequence of GAM501831 RNA and the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 1 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III, respectively. It is appreciated that the number of target binding sites shown in Fig. 1 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 1 shows target binding sites only in the 3'UTR region, these target binding sites may instead be located in the 5'UTR region or in both the 3'UTR and 5'UTR regions.

The complementary binding of GAM501831 RNA, herein designated GAM RNA to target binding sites on GAM501831 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits the translation of GAM501831 target RNA into respective GAM501831 target protein, herein designated GAM TARGET PROTEIN, shown surrounded by a broken line.

It is appreciated that the GAM501831 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM501831 target genes. The mRNA of each one of this plurality of GAM501831 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM501831 RNA, herein designated GAM RNA and which when bound by GAM501831 RNA causes inhibition of translation of the

GAM501831 target mRNA into a corresponding GAM501831 target protein.

The mechanism of the translational inhibition that is exerted by GAM501831

RNA, herein designated GAM RNA on one or more GAM501831 target genes, herein

collectively designated GAM TARGET GENE, may be similar or identical to the

known mechanism of translational inhibition exerted by known miRNA

oligonucleotides.

The nucleotide sequence of GAM501831 precursor RNA, herein designated GAM

PRECURSOR RNA, its respective genomic source and genomic location and a

schematic representation of a predicted secondary folding of GAM501831

folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA are set

forth in Tables 3-4, hereby incorporated herein.

The nucleotide sequences of a "diced" GAM501831 RNA, herein designated GAM

RNA from GAM501831 folded precursor RNA are set forth in Table 5, hereby

incorporated herein. The nucleotide sequences of target binding sites, such

as BINDING SITE I, BINDING SITE II and BINDING SITE III of Fig. 1, found on

GAM501831 target RNA, herein designated GAM TARGET RNA, and a schematic

representation of the complementarity of each of these target binding sites

to GAM501831 RNA, herein designated GAM RNA are set forth in Tables 6-7,

hereby incorporated herein.

It is appreciated that the specific functions and accordingly the utilities

of GAM501831 RNA are correlated with and may be deduced from the identity of

the GAM501831 target gene inhibited thereby, and whose functions are set

forth in Table 8, hereby incorporated herein.

Table 3, lines 320140-320141, shows data relating to the source and location of the GAM oligonucleotide, specifically the GAM

PRECURSOR (hairpin) and its position in the genomic sequence of Herpes virus 5.

GAM NAME	PRECUR GAM ORGANISM	SOURCE	STR SRC-START	SRC-END
SEQ-ID		AND OFFSET	AND OFFSET	OFFSET

GAM501831	420405	Human herpesvirus 5	NC 001347	+	164118	164184
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[210] The nucleotide sequence of GAM PRECURSOR RNAs, and a schematic representation of a predicted secondary folding of GAM FOLDED PRECURSOR RNAs, of each of a plurality of GAM oligonucleotides that are described by Fig. 1 are set forth in Table 4, hereby incorporated herein. Table 4, lines 599770-599773, shows a schematic representation of the GAM folded precursor as set forth in SEQ ID NO: 4204050, beginning at the 5' end (beginning of upper row) to the 3' end (beginning of lower row), where the hairpin loop is positioned at the right part of the drawing.

GAM NAME	PRECUR GAM	PRECURSOR-SEQUENCE	GAM FOLDED	PRECURSOR RNA
SEQ-ID ORGANISM				
GAM501831	4204050 Human	GACAGCCTCCGGATCACAIG	CC	A G C C CTGCCA
herpes virus 5 GTTACTCAGCGTCTGCCAGC GACAGCCT GGATC CAT GTTACT AG GT				
CTAAGTGACGGTGAGATCCA CTGTGGGA CCTAG GTG CAGTGA TC CG				
GGCTGTC				
A G A -				

[211] The nucleotide sequence of “diced” GAM RNAs of each of a plurality of GAM oligonucleotides that are described by Fig. 1 are set forth in Table 5, hereby incorporated herein. Table 5, lines 239916 and 239917 shows the mature GAM RNA as set forth in SEQ ID NO: 117937 as sliced by DICER from the GAM PRECURSOR sequence (hairpin) as set forth in SEQ ID NO: 4204050.

GAM NAME	GAM ORGANISM	GAM RNA SEQUENCE	PRECUR	GAM
GAM501831	Human herpesvirus 5	AGTGACGGTGAGATCCAGGCTG	4204050	A

[212] The nucleotide sequences of target binding sites, such as BINDING SITE I, BINDING SITE II, and BINDING SITE III, that are found on GAM TARGET RNAs of each of a plurality of GAM oligonucleotides that are described by Fig. 1, and a schematic representation of the complementarity of each of these target binding sites to each of a plurality of GAM RNAs that are described by Fig. 1 are set forth in Tables 6-7, hereby incorporated herein. Table 6 shows data relating to the SEQ ID NO: of the GAM target binding site

sequence to the TARGET gene name as bound by the GAM RNA as set forth in SEQ ID NO: 117937. Table 6, lines 2093282 and 2093283 relate to target binding site SEQ ID NO: 2034243; lines 6630926 and 6630927 relate to target binding site SEQ ID NO: 3983175; lines 2093540 and 2093541 relate to target binding site SEQ ID NO: 2034310; lines 6638580 and 6638581 relate to target binding site SEQ ID NO: 3985198; line 6630929 relates to target binding site SEQ ID NO: 3983175; line 2093543 relates to target binding site SEQ ID NO: 2034310; line 6638583 relates to target binding site SEQ ID NO: 3985198; lines 2087866 and 2087867 relate to target binding site SEQ ID NO: 2032849; lines 663308 and 663309 relate to target binding site SEQ ID NO: 3983798; and line 2058344 relates to SEQ ID NO: 2024974.

TARGET BINDING SITE SEQ ID	TARGET ORGANISM	TARGET	TARGET BINDING SITE SEQUENCE
2034243	Human herpesvirus 5	NC_001347 190696 - 19	GGGTGCACCTGCTGCCGCCACT
3983175	Human herpesvirus 5	NC_001347 190696 - 19	GGGTGCACCTGCTGCCGCCACT
2034310	Human herpesvirus 5	NC_001347 190696 - 19	GCTGATCGCCGTCACI
3985198	Human herpesvirus 5	NC_001347 190696 - 19	GCTGATCGCCGTCACI
3983175	Human herpesvirus 5	NP_040085.1 gene	GGGTGCACCTGCTGCCGCCACT
2034310	Human herpesvirus 5	NP_040085.1 gene	GCTGATCGCCGTCACI
3985198	Human herpesvirus 5	NP_040085.1 gene	GCTGATCGCCGTCACI

3983798	Human herpesvirus 5	NC_001347.5	4824 - 560	GTGCGCGTCACI
				95 gene

Table 7, lines 6493595-6493625 shows data relating to target-genes and binding sites of GAM oligonucleotides.

GAM NAME	GAM ORGANISM	GAM RNA	TARGET	TARGET	TARGET	REF-ID	ORGANISM	UTR BINDING SITE	DRAW (UPPER: GAM	POS	
=====											
SEQUENCE	BS-SEQ	TARGET	TARGET	TARGET	REF-ID	ORGANISM	TARGET;LOWER: GAM)	=====			
=====											
GAM501831	Human herpes virus 5	AGTGACGG CCGTGCAC	NC_001347	1	Human herpes virus 5	NC_001347	1	Human herpes virus 5	3	-- G C C GCTG C A	
AGGCTG	GCCACT	96 - 19	637					GC TG A CT	CCG CACT		
3236	ge							CG AC T GA	GGC GTGA		
ne								GT G C A GT--	A		
=====											
GAM501831	Human herpes virus 5	AGTGACGG CCGTGCAC	NP_0400	NC_001347	1	Human herpes virus 5	NC_001347	1	Human herpes virus 5	3	-- G C C GCTG C A
AGGCTG	GCCACT	96 - 19	637					GC TG A CT	CCG CACT		
3236	ge							CG AC I GA	GGC GTGA		
ne								GT G C A GT--	A		
=====											
GAM501831	Human herpes virus 5	AGTGACGG CCGTGCAC	NP_0400	NC_001347	1	Human herpes virus 5	NC_001347	1	Human herpes virus 5	3	-- G C C GCTG C A
AGGCTG	GCCACT	96 - 19	637					GC TG ATC	CCGTCACT		
3236	ge							CG AC TAG	GGCAGTGA		
ne								GT G C AGT			
=====											
GAM501831	Human herpes virus 5	AGTGACGG CCGTGCAC	NP_0400	NC_001347	1	Human herpes virus 5	NC_001347	1	Human herpes virus 5	3	-- G C C GCTG C A
AGGCTG	GCCACT	96 - 19	637					GC TG ATC	CCGTCACT		
3236	ge							CG AC TAG	GGCAGTGA		
ne								GT G C AGT			
=====											
GAM501831	Human herpes virus 5	AGTGACGG CCGTGCAC	NP_0400	NC_001347	1	Human herpes virus 5	NC_001347	1	Human herpes virus 5	3	-- G C C GCTG C A
AGGCTG	GCCACT	96 - 19	637					GC TG ATC	CCGTCACT		
3236	ge							CG AC TAG	GGCAGTGA		
ne								GT G C AGT			
=====											



	GT	G	C	AGT
GAM501831 Human herpes AGTGACGG GTCGCCGT NC_001347 5 Human herpes 3 -- - ----- A				
virus 5 TGAGATCC CACT 47 5482 4423 - 5482 virus 5 GTC G CCGTCACT				
AGGCTG 4 - 560 3 CGG C GGCAGTGA				
95 gene GT A CTAGAGT				
GAM501831 Human herpes GCCTCCGG TCCATCCT SFTPA1 NM_005411 Human 3 -- -- ----- T B				
virus 5 ATCACATG GAGGC T CCAT CC GAGGC				
GTTACT A GGTA GG CTCCG				
TC TT CACTA C				

[213] It is appreciated that the specific functions and accordingly the utilities of each of a plurality of GAM oligonucleotides that are described by Fig. 1 are correlated with and may be deduced from the identity of the GAM TARGET GENES inhibited thereby, and whose functions are set forth in Table 8, hereby incorporated herein Table 8C, lines 4766438-4766618 shows data relating to the function and utilities of GAM RNA as set forth in SEQ ID NO: 117937.

GAM NAME	GAM RNA	GAM ORGANISM	TARGET	TARGET	GAM FUNCTION	GAM
SEQUENCE		ORGANISM				POS
=====	=====	=====	=====	=====	=====	=====
GAM501831 AGTGACGG Human herpes NC_001347 Human herpes	47 1906 pesvirus	d by the Human herpesvirus 5 genome, which targets a viral tar				A
AGGCTG	96 - 19 5	get gene NC_001347 190696 - 193236 gene (UTR reference: NC_001				
	3236 ge	347 193237 - 193637) as part of an internal viral regulation m				
	ne	echanism.				
		NC_001347 190696 - 193236 gene BINDING SITE 1 and NC_001347 19				
		0696 - 193236 gene BINDING SITE 2 are viral target binding sit				
		es that are found in the untranslated regions of mRNA encoded				
		by the NC_001347 190696 - 193236 gene gene, corresponding to t				
		arget binding sites such as BINDING SITE I, BINDING SITE II or				
		BINDING SITE III of Fig. 1. The nucleotide sequences of NC_00				
		1347 190696 - 193236 gene BINDING SITE 1 and NC_001347 190696				
		- 193236 gene BINDING SITE 2, and the complementary secondary				

structure to the nucleotide sequence of GAM501831 RNA are set forth in Tables 6-7, hereby incorporated herein.

A function of GAM501831 is to inhibit NC\_001347 190696 - 193236 gene, a GAM501831 viral target gene which is associated with Human herpesvirus 5 infection, as part of an internal viral regulation mechanism. Accordingly, the utilities of GAM501831 include the diagnosis, prevention and treatment of Human herpesvirus 5 infection and associated clinical conditions.

GAM501831 AGTGACGG Human herpes NC\_001347 Human herpesvirus 5 47 1906 pesvirus d by the Human herpesvirus 5 genome, which targets a viral target gene NC\_001347 190696 - 193236 gene (UTR reference: NC\_001347 190696 - 193236 gene) as part of an internal viral regulation mechanism.

NC\_001347 190696 - 193236 gene BINDING SITE 1 and NC\_001347 190696 - 193236 gene BINDING SITE 2 are viral target binding sites that are found in the untranslated regions of mRNA encoded by the NC\_001347 190696 - 193236 gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of NC\_001347 190696 - 193236 gene BINDING SITE 1 and NC\_001347 190696 - 193236 gene BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM501831 RNA are set forth in Tables 6-7, hereby incorporated herein.

Another function of GAM501831 is to inhibit NC\_001347 190696 - 193236 gene, a GAM501831 viral target gene which is associated with Human herpesvirus 5 infection, as part of an internal viral regulation mechanism. Accordingly, the utilities of GAM501831

1831 include the diagnosis, prevention and treatment of Human herpesvirus 5 infection and associated clinical conditions.

GAM501831 AGTGACGG Human herpes NC\_001347 Human herpesvirus 5 genome, which targets a viral target site that is a found in the 3' untranslated region of mRNA encoded by the NC\_001347 54824 - 56095 gene, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of NC\_001347 54824 - 56095 gene BINDING SITE, and the complementary secondary structure to the nucleotide sequence of GAM501831 RNA are set forth in Tables 6-7, hereby incorporated herein.

Another function of GAM501831 is to inhibit NC\_001347 54824 - 56095 gene, a GAM501831 viral target gene which is associated with Human herpesvirus 5 infection, as part of an internal viral regulation mechanism. Accordingly, the utilities of GAM501831 include the diagnosis, prevention and treatment of Human herpesvirus 5 infection and associated clinical conditions.

GAM501831 AGTGACGG Human herpes NC\_001347 Human herpesvirus 5 genome, which targets a viral target site that is a found in the 3' untranslated region of mRNA encoded by the NC\_001347 54824 - 56095 gene, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of NC\_001347 54824 - 56095 gene BINDING SITE, and the complementary secondary structure to the nucleotide sequence of GAM501831 RNA are set forth in Tables 6-7, hereby incorporated herein.

GAM501831 AGTGACGG Human herpes NP\_0400 Human herpesvirus 5 genome, which targets a viral target gene NP\_040085.1 gene (UTR reference: NC\_001347 193237 - 193637) as part of an internal viral regulation mechanism.

NP\_040085.1 gene BINDING SITE I and NP\_040085.1 gene BINDING SITE II are viral target binding sites that are found in the untranslated regions of mRNA encoded by the NP\_040085.1 gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of NP\_040085.1 gene BINDING SITE I and NP\_040085.1

gene BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM501831 RNA are set forth in

Tables 6-7, hereby incorporated herein.

Another function of GAM501831 is to inhibit NP\_040085.1 gene, a GAM501831 viral target gene which is associated with Human herpesvirus 5 infection, as part of an internal viral regulation mechanism. Accordingly, the utilities of GAM501831 include the diagnosis, prevention and treatment of Human herpesvirus 5 infection and associated clinical conditions.

GAM501831 AGTACGCGG Human herpes NP\_0400 Human herpesvirus 5 is a viral miRNA-like oligonucleotide that is encoded by

AGGCTG 5' TGAGATCC virus 5 85.1 gene (UTR reference: NC\_001347 193237 - 1

93637) as part of an internal viral regulation mechanism. NP\_040085.1 gene BINDING SITE 1 and NP\_040085.1 gene BINDING SITE 2

are viral target binding sites that are found in the untranslated regions of mRNA encoded by the NP\_040085.1 gene

, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide

sequences of NP\_040085.1 gene BINDING SITE 1 and NP\_040085.1 gene BINDING SITE 2, and the complementary secondary structure

to the nucleotide sequence of GAM501831 RNA are set forth in

Tables 6-7, hereby incorporated herein.

Another function of GAM501831 is to inhibit NP\_040085.1 gene, a GAM501831 viral target gene which is associated with Human

herpesvirus 5 infection, as part of an internal viral regulation mechanism. Accordingly, the utilities of GAM501831 include the

diagnosis, prevention and treatment of Human herpesvirus 5

infection and associated clinical conditions.

GAM501831 GCCTCCGG Human herpes SFTPAl Human GAM501831 is a viral miRNA-like oligonucleotide that is encode B  
ATCACATG virus 5 d by the Human herpesvirus 5 genome, which targets a human hos  
GTTACT t gene Surfactant, pulmonary- associated protein A1 (SFTPAl, A  
cession number: NM\_005411) as part of a viral host-attacking  
mechanism.  
SFTPAl BINDING SITE is a human target binding site that is a f  
ound in the the 3' untranslated region of mRNA encoded by the  
SFTPAl gene, corresponding to a target binding site such as BI  
NDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. I  
he nucleotide sequences of SFTPAl BINDING SITE, and the comple  
mentary secondary structure to the nucleotide sequence of GAM5  
01831 RNA are set forth in Tables 6-7, hereby incorporated her  
ein.  
Another function of GAM501831 is to inhibit SFTPAl, a GAM50183  
1 human target gene which is involved in lipids and carbohydra  
tes metabolism. SFTPAl is associated with Human herpesvirus 5  
infection, and therefore GAM501831 is associated with the abo  
vementioned infection, as part of a novel viral mechanism of a  
ttacking a host. Accordingly, the utilities of GAM501831 inclu  
de the diagnosis, prevention and treatment of Human herpesviru  
s 5 infection and associated clinical conditions.  
The function of SFTPAl and its association with various diseas  
es and clinical conditions has been established by previous st  
udies, as described hereinabove with reference to GAM336913.

GAM501831 GCCTCCGG Human herpes SFTPAl Human GAM501831 is a viral miRNA-like oligonucleotide that is encode B

ATCACAIG virus 5  
GTTACT

d by the Human herpesvirus 5 genome, which targets a human host gene Surfactant, pulmonary-associated protein A1 (SFTPA1, A ccession number: NM\_005411) as part of a viral host-attacking mechanism.

SFTPA1 BINDING SITE is a human target binding site that is a found in the the 3' untranslated region of mRNA encoded by the SFTPA1 gene, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of SFTPA1 BINDING SITE, and the complementary secondary structure to the nucleotide sequence of GAM501831 RNA are set forth in Tables 6-7, hereby incorporated herein.

Another function of GAM501831 is to inhibit SFTPA1, a GAM501831 human target gene which is involved in lipids and carbohydrate metabolism. SFTPA1 is associated with Human herpesvirus 5 infection, and therefore GAM501831 is associated with the above mentioned infection, as part of a novel viral mechanism of attacking a host. Accordingly, the utilities of GAM501831 include the diagnosis, prevention and treatment of Human herpesvirus 5 infection and associated clinical conditions.

The function of SFTPA1 and its association with various diseases and clinical conditions has been established by previous studies, as described hereinabove with reference to GAM336913.

[214] Studies documenting the well known correlations between each of a plurality of GAM TARGET GENES that are described by Fig. 1 and the known gene functions and related discusses are listed in Table 9, hereby incorporated herein. Figure 9, lines 40832-40882, shows the GAM target genes and information related to the target gene.

SFTPA1 Human Bruns, G.; Stroh, H.; Veldman, G. M.; Latt, S. A.; Floros, J.: The 35 kd pulmonary surfactant-associated protein is encoded on chromosome 10. Hum. Genet.

76: 58-62, 1987.

SFTPA1 Human Fisher, J. H.; Kao, F. T.; Jones, C.; White, R. T.; Benson, B. J.; Mason, R. J.:  
The coding sequence for the 32,000-dalton pulmonary surfactant-associated  
protein A is located on chromosome 10 and identifies two separate  
restriction-fragment-length polymorphisms. Am. J. Hum. Genet. 40: 503-511, 1987.

SFTPA1 Human Floros, J.; DiAngelo, S.; Koptides, M.; Karinch, A. M.; Rogan, P. K.; Nielsen,  
H.; Spragg, R. G.; Watterberg, K.; Deiter, G.: Human SP-A locus: allele  
frequencies and linkage disequilibrium between the two surfactant protein A  
genes. Am. J. Resp. Cell Molec. Biol. 15: 489-498, 1996.

SFTPA1 Human Floros, J.; Hoover, R. R.: Genetics of the hydrophilic surfactant proteins A and  
D. Biochim. Biophys. Acta 1408: 312-322, 1998.

SFTPA1 Human Glasser, S. W.; Korfhagen, T. R.; Weaver, I.; Pilot-Matias, I.; Fox, J. L.;  
Whitsett, J. A.: cDNA and deduced amino acid sequence of human pulmonary  
surfactant-associated proteolipid SPL(Phe). Proc. Nat. Acad. Sci. 84: 4007-4011,  
1987.

SFTPA1 Human Haataja, R.; Ramet, M.; Marttila, R.; Hallman, M.: Surfactant proteins A and B  
as interactive genetic determinants of neonatal respiratory distress syndrome.  
Hum. Molec. Genet. 9: 2751-2760, 2000.

SFTPA1 Human Kolble, K.; Lu, J.; Mole, S. E.; Kaluz, S.; Reid, K. B. M.: Assignment of the  
human pulmonary surfactant protein D gene (SFTPD) to 10q22-q23 close to the  
surfactant protein A gene cluster. Genomics 17: 294-298, 1993.

SFTPA1 Human Latt, S. A.: Personal Communication. Boston, Mass. 6/3/1987.



SFTPA1	Human	Moore, K. J.; D'Amore-Bruno, M. A.; Korfhagen, T. R.; Glasser, S. W.; Whitsett, J. A.; Jenkins, N. A.; Copeland, N. G.: Chromosomal localization of three pulmonary surfactant protein genes in the mouse. <u>Genomics</u> 12: 388-393, 1992.
SFTPA1	Human	Ramet, M.; Haataja, R.; Marttila, R.; Floros, J.; Hallman, M.: Association between the surfactant protein A (SP-A) gene locus and respiratory-distress syndrome in the Finnish population. <u>Am. J. Hum. Genet.</u> 66: 1569-1579, 2000.
SFTPA1	Human	Ramet, M.; Lofgren, J.; Albo, O.-P.; Hallman, M.: Surfactant protein-A gene locus associated with recurrent otitis media. <u>J. Pediatr.</u> 138: 266-268, 2001.
SFTPA1	Human	Selman, M.; Lin, H.-M.; Montano, M.; Jenkins, A. L.; Estrada, A.; Lin, Z.; Wang, G.; DiAngelo, S. L.; Guo, X.; Umstead, T. M.; Lang, C. M.; Pardo, A.; Phelps, D. S.; Floros, J.: Surfactant protein A and B genetic variants predispose to idiopathic pulmonary fibrosis. <u>Hum. Genet.</u> 113: 542-550, 2003.
SFTPA1	Human	White, R. T.; Damm, D.; Miller, J.; Spratt, K.; Schilling, J.; Hawgood, S.; Benson, B.; Cordell, B.: Isolation and characterization of the human pulmonary surfactant apoprotein gene. <u>Nature</u> 317: 361-363, 1985. --